

SEQUENCE LISTING

<110> Max Planck Gesellschaft zur Förderung der Wissensc

<120> Substance binding human IgG Fc receptor IIb

<130> 30287P-EP

<140>

<141>

<160> 11

<170> PatentIn Ver. 2.1

<210> 1

<211> 172

<212> PRT

<213> Human

<400> 1

Ala Pro Pro Lys Ala Val Leu Lys Leu Glu Pro Pro Trp Ile Asn Val
1 5 10 15

Leu Gln Glu Asp Ser Val Thr Leu Thr Cys Gln Gly Ala Arg Ser Pro
20 25 30

Glu Ser Asp Ser Ile Gln Trp Phe His Asn Gly Asn Leu Ile Pro Thr
35 40 45

His Thr Gln Pro Ser Tyr Arg Phe Lys Ala Asn Asn Asn Asp Ser Gly
50 55 60

Glu Tyr Thr Cys Gln Thr Gly Gln Thr Ser Leu Ser Asp Pro Val His
65 70 75 80

Leu Thr Val Leu Ser Glu Trp Leu Val Leu Gln Thr Pro His Leu Glu
85 90 95

Phe Gln Glu Gly Glu Thr Ile Met Leu Arg Cys His Ser Trp Lys Asp
100 105 110

Lys Pro Leu Val Lys Val Thr Phe Phe Gln Asn Gly Lys Ser Gln Lys
115 120 125

Phe Ser Arg Leu Asp Pro Thr Phe Ser Ile Pro Gln Ala Asn His Ser
130 135 140

His Ser Gly Asp Tyr His Cys Thr Gly Asn Ile Gly Tyr Thr Leu Phe
145 150 155 160

Ser Ser Lys Pro Val Thr Ile Thr Val Gln Val Pro
165 170

<210> 2

<211> 172

<212> PRT

<213> Human

<400> 2

Ala Pro Pro Lys Ala Val Leu Lys Leu Glu Pro Gln Trp Ile Asn Val

2/7

1	5	10	15
Leu Gln Glu Asp Ser Val Thr Leu Thr Cys Arg Gly Thr His Ser Pro	20	25	30
Glu Ser Asp Ser Ile Gln Trp Phe His Asn Gly Asn Leu Ile Pro Thr	35	40	45
His Thr Gln Pro Ser Tyr Arg Phe Lys Ala Asn Asn Asn Asp Ser Gly	50	55	60
Glu Tyr Thr Cys Gln Thr Gly Gln Thr Ser Leu Ser Asp Pro Val His	65	70	75
Leu Thr Val Leu Ser Glu Trp Leu Val Leu Gln Thr Pro His Leu Glu	85	90	95
Phe Gln Glu Gly Glu Thr Ile Val Leu Arg Cys His Ser Trp Lys Asp	100	105	110
Lys Pro Leu Val Lys Val Thr Phe Phe Gln Asn Gly Lys Ser Lys Lys	115	120	125
Phe Ser Arg Ser Asp Pro Asn Phe Ser Ile Pro Gln Ala Asn His Ser	130	135	140
His Ser Gly Asp Tyr His Cys Thr Gly Asn Ile Gly Tyr Thr Leu Tyr	145	150	155
Ser Ser Lys Pro Val Thr Ile Thr Val Gln Ala Pro	165	170	

<210> 3
 <211> 13
 <212> PRT
 <213> Human

<400> 3
 Ser Lys Lys Phe Ser Arg Ser Asp Pro Asn Phe Ser Gly
 1 5 10

<210> 4
 <211> 312
 <212> DNA
 <213> hybridoma

<220>
 <221> CDS
 <222> (1)..(312)

<400> 4
 aga att cag ctg acc cag tct cca tcc tcc tta tct gcc tct ctg gga 48
 Arg Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Leu Gly
 1 5 10 15

gaa aga gtc agt ctc act tgt cgg gca agt cag gaa att agt ggt tac 96
 Glu Arg Val Ser Leu Thr Cys Arg Ala Ser Gln Glu Ile Ser Gly Tyr
 20 25 30

3/7

tta agc tgg ctt cag cag aaa cca gat gga act att aaa cgc ctg atc 144
 Leu Ser Trp Leu Gln Gln Lys Pro Asp Gly Thr Ile Lys Arg Leu Ile
 35 40 45
 tac gcc aca tcc gct tta gat tct ggt gtc cca aaa agg ttc agt ggc 192
 Tyr Ala Thr Ser Ala Leu Asp Ser Gly Val Pro Lys Arg Phe Ser Gly
 50 55 60
 agt ggg tct ggg tca aat tat tct ctc acc atc agc agc ctt gag tct 240
 Ser Gly Ser Gly Ser Asn Tyr Ser Leu Thr Ile Ser Ser Leu Glu Ser
 65 70 75 80
 gaa gat ttt gca gac tat tac tgt cta caa tat gct aat tat ccg tac 288
 Glu Asp Phe Ala Asp Tyr Tyr Cys Leu Gln Tyr Ala Asn Tyr Pro Tyr
 85 90 95
 acg ttc gga ggg ggg acc aag ctg 312
 Thr Phe Gly Gly Gly Thr Lys Leu
 100

<210> 5
 <211> 104
 <212> PRT
 <213> hybridoma

<400> 5
 Arg Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Leu Gly
 1 5 10 15
 Glu Arg Val Ser Leu Thr Cys Arg Ala Ser Gln Glu Ile Ser Gly Tyr
 20 25 30
 Leu Ser Trp Leu Gln Gln Lys Pro Asp Gly Thr Ile Lys Arg Leu Ile
 35 40 45
 Tyr Ala Thr Ser Ala Leu Asp Ser Gly Val Pro Lys Arg Phe Ser Gly
 50 55 60
 Ser Gly Ser Gly Ser Asn Tyr Ser Leu Thr Ile Ser Ser Leu Glu Ser
 65 70 75 80
 Glu Asp Phe Ala Asp Tyr Tyr Cys Leu Gln Tyr Ala Asn Tyr Pro Tyr
 85 90 95
 Thr Phe Gly Gly Gly Thr Lys Leu
 100

<210> 6
 <211> 312
 <212> DNA
 <213> hybridoma

<220>
 <221> CDS
 <222> (1)..(312)

<400> 6
 gtg cag ctg cag cag tct gga cct gag ctg gtg aag cct ggg gct tca 48
 Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala Ser
 1 5 10 15

gtg aag att tcc tgc aag gct tct ggc tac acc ttc act gac tac tat 96
Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Tyr
20 25 30

ata tac tgg gtg aaa cag tgg cct gga cag gga ctt gag tgg att gga 144
Ile Tyr Trp Val Lys Gln Trp Pro Gly Gln Gly Leu Glu Trp Ile Gly
35 40 45

tgg att ttt cct gga act ggt aat act tac tac aat gaa aac ttc aag 192
Trp Ile Phe Pro Gly Thr Gly Asn Thr Tyr Tyr Asn Glu Asn Phe Lys
50 55 60

gac aag gcc aca ctt act ata gat aga tcc tcc agc aca gcc tac atg 240
Asp Lys Ala Thr Leu Thr Ile Asp Arg Ser Ser Ser Thr Ala Tyr Met
65 70 75 80

ttg ctc ggc agc ctg acc tct gag gac tct gcg gtc tat ttc tgt tat 288
Leu Leu Gly Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys Tyr
85 90 95

ggt ccg ttt gct tac tgg ggc caa 312
Gly Pro Phe Ala Tyr Trp Gly Gln
100

<210> 7
<211> 104
<212> PRT
<213> hybridoma

<400> 7
Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala Ser
1 5 10 15
Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Tyr
20 25 30
Ile Tyr Trp Val Lys Gln Trp Pro Gly Gln Gly Leu Glu Trp Ile Gly
35 40 45
Trp Ile Phe Pro Gly Thr Gly Asn Thr Tyr Tyr Asn Glu Asn Phe Lys
50 55 60
Asp Lys Ala Thr Leu Thr Ile Asp Arg Ser Ser Ser Thr Ala Tyr Met
65 70 75 80
Leu Leu Gly Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys Tyr
85 90 95
Gly Pro Phe Ala Tyr Trp Gly Gln
100

<210> 8
<211> 331
<212> DNA
<213> hybridoma

<220>
<221> CDS
<222> (1)..(330)

<400> 8

```

aga att cag ctg acc cag tct cct gct tcc tta gct gta tct ctg ggg      48
Arg Ile Gln Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly
  1           5           10           15

cag agg gcc acc atc tca tac agg gcc agc aaa agt gtc agt aca tct      96
Gln Arg Ala Thr Ile Ser Tyr Arg Ala Ser Lys Ser Val Ser Thr Ser
          20           25           30

ggc tat agt tat atg cac tgg aac caa cag aaa cca gga cag cca ccc      144
Gly Tyr Ser Tyr Met His Trp Asn Gln Gln Lys Pro Gly Gln Pro Pro
          35           40           45

aga ctc ctc atc tat ctt gta tcc aac cta gaa tct ggg gtc cct gcc      192
Arg Leu Leu Ile Tyr Leu Val Ser Asn Leu Glu Ser Gly Val Pro Ala
          50           55           60

agg ttc agt ggc agt ggg tct ggg aca gac ttc acc ctc aac atc cat      240
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His
          65           70           75           80

cct gtg gag gag gag gat gct gca acc tat tac tgt cag cac att agg      288
Pro Val Glu Glu Glu Asp Ala Ala Thr Tyr Tyr Cys Gln His Ile Arg
          85           90           95

gag ctt aca cgt tcg gag ggg gga cca agc tgg aga tct aac a          331
Glu Leu Thr Arg Ser Glu Gly Gly Pro Ser Trp Arg Ser Asn
          100           105           110

```

<210> 9

<211> 110

<212> PRT

<213> hybridoma

<400> 9

```

Arg Ile Gln Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly
  1           5           10           15

Gln Arg Ala Thr Ile Ser Tyr Arg Ala Ser Lys Ser Val Ser Thr Ser
          20           25           30

Gly Tyr Ser Tyr Met His Trp Asn Gln Gln Lys Pro Gly Gln Pro Pro
          35           40           45

Arg Leu Leu Ile Tyr Leu Val Ser Asn Leu Glu Ser Gly Val Pro Ala
          50           55           60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His
          65           70           75           80

Pro Val Glu Glu Glu Asp Ala Ala Thr Tyr Tyr Cys Gln His Ile Arg
          85           90           95

Glu Leu Thr Arg Ser Glu Gly Gly Pro Ser Trp Arg Ser Asn
          100           105           110

```

<210> 10

<211> 343

<212> DNA

<213> hybridoma

<220>

<221> CDS

<222> (1)..(342)

<400> 10

gtg	cag	ctg	cag	gag	tct	gga	cct	ggc	ctg	gtg	gcg	ccc	tca	cag	agc	48
Val	Gln	Leu	Gln	Glu	Ser	Gly	Pro	Gly	Leu	Val	Ala	Pro	Ser	Gln	Ser	
1				5					10					15		
ctg	tcc	atc	aca	tgc	acc	gtc	tca	ggg	ttc	tca	tta	act	agc	tat	ggc	96
Leu	Ser	Ile	Thr	Cys	Thr	Val	Ser	Gly	Phe	Ser	Leu	Thr	Ser	Tyr	Gly	
			20					25					30			
gta	cac	tgg	gtt	cgc	cag	cct	cca	gga	aag	ggc	ctg	gag	tgg	ctg	gta	144
Val	His	Trp	Val	Arg	Gln	Pro	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Leu	Val	
		35					40					45				
gtg	ata	tgg	agt	gat	gga	agc	aca	acc	tat	aat	tca	gct	ctc	aaa	tcc	192
Val	Ile	Trp	Ser	Asp	Gly	Ser	Thr	Thr	Tyr	Asn	Ser	Ala	Leu	Lys	Ser	
	50					55					60					
aga	ctg	agc	atc	agc	aag	gac	aac	tcc	aag	agc	caa	gtt	ttc	tta	aaa	240
Arg	Leu	Ser	Ile	Ser	Lys	Asp	Asn	Ser	Lys	Ser	Gln	Val	Phe	Leu	Lys	
65					70				75						80	
atg	aac	agt	ctc	caa	act	gat	gac	aca	gcc	atg	tac	tac	tgt	gcc	aga	288
Met	Asn	Ser	Leu	Gln	Thr	Asp	Asp	Thr	Ala	Met	Tyr	Tyr	Cys	Ala	Arg	
				85				90						95		
gag	cct	ccc	acg	acg	tac	gtt	tgc	tta	ctg	ggg	cca	agg	gac	cac	tct	336
Glu	Pro	Pro	Thr	Thr	Tyr	Val	Cys	Leu	Leu	Gly	Pro	Arg	Asp	His	Ser	
			100				105						110			
aga	tta	a														343
Arg	Leu															

<210> 11

<211> 114

<212> PRT

<213> hybridoma

<400> 11

Val	Gln	Leu	Gln	Glu	Ser	Gly	Pro	Gly	Leu	Val	Ala	Pro	Ser	Gln	Ser
1				5					10					15	
Leu	Ser	Ile	Thr	Cys	Thr	Val	Ser	Gly	Phe	Ser	Leu	Thr	Ser	Tyr	Gly
			20					25					30		
Val	His	Trp	Val	Arg	Gln	Pro	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Leu	Val
		35					40					45			
Val	Ile	Trp	Ser	Asp	Gly	Ser	Thr	Thr	Tyr	Asn	Ser	Ala	Leu	Lys	Ser
	50					55					60				
Arg	Leu	Ser	Ile	Ser	Lys	Asp	Asn	Ser	Lys	Ser	Gln	Val	Phe	Leu	Lys
65					70				75						80
Met	Asn	Ser	Leu	Gln	Thr	Asp	Asp	Thr	Ala	Met	Tyr	Tyr	Cys	Ala	Arg
				85				90						95	

Glu Pro Pro Thr Thr Tyr Val Cys Leu Leu Gly Pro Arg Asp His Ser
100 105 110

Arg Leu